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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prime.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_032802:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT:
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLNHHIRLTISALLTALLVT.....FLWVKPYRPKNLSFYLTAKA 111
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
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                                         AAB60640
AAY81582
AAB793269
AAG31852
AAG31851
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    AAR95910
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                                     Amino acid sequenc
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrha
Streptococcus pneu
Neisseria meningit
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Drosophila melanog	ABB66745	22	787	11.0	61.5	5
	В	22	787	11.0	61.5	44
		22	787	11.0	61.5	3
melano	ABB58186	22	787	•	61.5	2
	ABB66746	22	465		61.5	1
а П	ABB71901	22	214	٠	61.5	ô
s thali	AAG29455	21	330	٠	62	39
Chlamydia pneumoni	AAY35229	20	330	11.1	62	8
Arabidopsis thalia	AAG29456	21	326		62	37
Novel human diagno	ABG01105	22	999			36
ACNV DNA polymeras	AAB46720	22	782		N. 3	35
Novel human diagno	ABG01104	22	363	11.2	62.5	4
C glutamicum prote	AAG91022	22	255		N3	ພ
	AAG36451	21	1275	•	63	32
Arabidopsis thalia	AAG36452	21	1257	٠	63	3
Arabidopsis thalia	AAG36453	21	1222	•	63	ö
Porphorymonas ging	AAY34352	20	985	٠	63	29
Porphorymonas ging	AAY34476	20	981	11.3	63	28
HpaI restriction e	AAR32076	14	254	•	63	27
Human prostate can	AAB63940	22	196	•		8
Arabidopsis thalia	AAG54259	21	453	•	441	25
Arabidopsis thalia	AAG54260	21	430	٠	w	24
bidopsis	AAG54261	21	429	11.4	63.5	23
H. pylori GHPO 558	AAW98234	19	389	11.4	w	22
Human DNase, Homo	AAR06323	1	346	•	w	21
Corynebacterium gl	961	22	296		(4)	20
tamicu	214	22	295		(a)	9
Amino acid sequenc	754	22	970		64	8
n down-regula	-	21	2785	٠	64.5	17
엺	35	22	564		64.5	9
sativa rdrl	35	22	281		64.5	5
Human polypeptide	60	22	475	٠	66	7
n polyp	981	22	421	11.8	66	<u>ω</u>
Novel human diagno	ABG02873	22	222		66.5	12

ALIGNMENTS

RESULT AAB60640 YOUR X PRESENTED TO THE PRESENTATION OF THE PR BASB122 protein; strain ATCC43617; antigen; antibody; vaccine; genetic immunisation; infection; upper respiratory tract; otitis media; hearing logs; deafness; pneumonia; sinusttis; nosocomial infection; invasive disease; antibacterial; auditory. 30-JUL-1999; 30-JUL-1999; 31-JUL-2000; 2000WO-EP07365 08-FEB-2001. Moraxella catarrhalis strain ATCC43617 BASB122 protein 02-MAY-2001 AAB60640; AAB60640 standard; Protein; 111 AA Thonnard WO200109337-A2. Moraxella catarrhalis. (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. L J, (first entry) 99GB-0018034. 99GB-0018036.

' 3

Opacity

WPI; 2001-159874/16. N-PSDB; AAF59778.

New BASB122 and BASB124 polypeptides and polynucleotides from Moraxella

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RESULT
AAY81582
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compositions comporising an anti-BASB122 or anti-BASB124 antibody, and a method of identifying a Moraxella catarrhalis infection via the detection of BASB122 or BASB124 proteins or antibodies. The vaccine compositions of the invention are useful as prophylactic or therapeutic agents against Moraxella catarrhalis infections in mammals, particularly humans. Moraxella catarrhalis is a Gram negative bacterium frequently isolated from the human upper respiratory tract, which is responsible for several pathological conditions. It is responsible for about 15% of otitis media cases in children (which can lead to temporary or permanent hearing loss). It also causes pneumonia in elderly people, and sinusitis, nosocomial infections and, less frequently, invasive diseases. BASB122 or BASB124 proteins or nucleotides may additionally be used in screening for novel antibacterial compounds, and in the diagnosis and staging of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention also relates to immunogenic fragments of the BASB122 and BASB124 proteins, expression vectors and host cells comprising BASB122 or BASB124 nucleic acids, the recombinant production of BASB122 or BASB124, vaccine compositions comprising the BASB122 or BASB124 proteins or nucleic acids, an antibody against BASB122 or BASB124, therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the Moraxella catarrhalis strain ATCC43617 BASB122 and BASB124 proteins (AAB60640 and AAB60641, respectively) and to DNA encoding them (AAF59778 and AAF59779, respectively). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catarrhalis strain ATCC 43617, useful as the
rapeutic agents or vaccines against bacterial infections, e.g. otit
is media or pneumonia \, -
Gilbert CFG,
                              (MICR-) MICROBIAL TECHNICS LTD
                                                                  27-JUL-1998;
19-MAR-1999;
                                                                                                                     27-JUL-1999;
                                                                                                                                                        10-FEB-2000
                                                                                                                                                                                          WO200006737-A2
                                                                                                                                                                                                                          Streptococcus pneumoniae.
                                                                                                                                                                                                                                                           pneumococcal disease.
                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagno
                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae type 4 protein sequence #82
                                                                                                                                                                                                                                                                                                                                                                24 -MAY - 2000
                                                                                                                                                                                                                                                                                                                                                                                                 AAY81582;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY81582 standard; Protein; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infections. The present s
strain ATCC43617 BASB122
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
Hansbro
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                                                               98GB-0016337.
99US-0125164.
                                                                                                                     99WO-GB02451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 558; DB 22;
Pred. No. 3.9e-61;
D; Mismatches 0;
                                                                                                                                                                                                                                                                           infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Query Match Best Local Matches

36; Conser

Conservative

18;

Score 78; DB Pred. No. 0.36 18; Mismatches

0.36;

DB 21; Length 300 39;

Indels

34;

Gaps

6;

14.0%;

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isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05514 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               or inhibiting expression of the protein
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                                                                                                                                                                                                                                                                                                                                                                 Page 80; 108pp; English.
300 AA;
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                                                                                                                                                                                                                                                                                              RESULT
                                      Thonnard
                                                                                                                       03-AUG-2000
                                                                                                                                          WO200044904-A1
                                                                                                                                                            Neisseria meningitidis
                                                                                                                                                                                 bacteraemia;
                                                                                                                                                                                           BASB059;
                                                                                                                                                                                                             Neisseria meningitidis BASB059 protein.
                                                                                                                                                                                                                                  19-JAN-2001
                                                                                                                                                                                                                                                      AAB21107;
                                                                                                                                                                                                                                                                          AAB21107 standard; Protein; 112 AA
                                                                              29-JAN-1999;
                                                                                                  25-JAN-2000;
                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                    138
                                                                                                                                                                                                                                                                                                                            191
                                                                                                                                                                                                                                                                                                                                               104 SFYLTAK 110
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                                                                                                                                                                                                                                                                                                                                                                   nesilslhfledtlgwvavilmaivlrftdwyildp-----llslvisffilskalpr-- 190
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                                                                                                                                                                                                                                                                                                                                                                                                          lgalvtavilvtgsvlvilenvtkilhpqpvndegilwlgiiaitinllaslvvgkgktk 137
                                                                                                                                                                                           respiratory tract infection; invasive bacterial disease;
                                                                                                                                                                                 meningitis.
                                                                                                 2000WO-EP00561
                                                                                                                                                                                                                                  (first entry)
                                                                              99GB-0002070
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WPI; 2000-505978/45. N-PSDB; AAA76029.

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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                       Aujame L, B
Tinsley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the Neisseria meningitidis BASB059 protein. protein, its gene, agonists and antagonists can be used in diagnost assays for the bacterium, as vaccines to prevent infection and as treatments for bacterial infection, particularly those caused by Neisseria meningitidis, such as upper respiratory tract infections, invasive bacterial diseases, bacteraemia and meningitis.
                                            The present sequence represents a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that overexpress it, or express it in a non-toxic mutant form.
                                                                                                                                                                                                                              Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200026375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathogenic strain;
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    Sequence
                                                                                                                                                                                                                                                                      New polypeptide specific or preventative vaccines
                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1999;
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                                                                                                                                                                                                                       Page 69-70; 187pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 61;
                                                                                                                                                                                                                                                                                                                                                                                                         Bouchardon
Perrin A;
       112
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19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
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05-MAY-1999;
06-MAY-1999;
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07-MAY-1999;
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16-APR-1999;

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21-APR-1999;

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28-APR-1999;

30-APR-1999;
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05-MAR-1999
09-MAR-1999;
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3-0132407 3-0132484

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Arabidopsis thaliana
                                                                                                                                   AAG31852 standard;
Arabidopsis thaliana
                                           Protein identification;
                               hybridisation assay;
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20; Conservative
                     sequence
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                                                                                                                                   Protein;
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                               genetic mapping; gene
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908-014519 908-014519 908-014529 908-014529 908-014529 908-014591 908-014591 908-014638 908-014638 908-014730	9US-0143542 9US-0144085 9US-0144085 9US-0144085 9US-0144325 9US-0144332 9US-0144332 9US-0144332 9US-0144334 9US-0144334 9US-0144352 9US-0144814 9US-0145086 9US-0145086	99US-0139458. 99US-0139460. 99US-0139461. 99US-0139462. 99US-0139463. 99US-0139750. 99US-0139817. 99US-0139817. 99US-014053. 99US-014053. 99US-014054. 99US-014055. 99US-0141842. 99US-0142055. 99US-0142055. 99US-0142055. 99US-0142053. 99US-0142053.	9US-013722 9US-013752 9US-013772 9US-013772 9US-013804 9US-013884 9US-013941 9US-013945 9US-013945 9US-013945 9US-013945

S-0147192. S-0147260. S-0147303.

Query Match 12.5 Best Local Similarity 23.5 Matches 36; Conservative

12.5%; 26; Score Pred.

Mismatches 69.5; No. 4.

Indels Length

Gaps

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DB 38;

335; 55;

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9905-014831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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990S-0126785.
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99US-0125788.
99US-0126264.
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genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 12.5%;
1 Similarity 23.2%;
36; Conservative 2
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b; Pred. No. 4.7;
26; Mismatches
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Length Indels

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09-MAR-1999
23-MAR-1999
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1 Similarity 28.8%;
17; Conservative 18
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99US-0123180
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Pred. No. 6.8;
18; Mismatches
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28-CCT-1999;
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1 Similarity 28.8
17; Conservative
                                                                                 99US-0147935.
99US-0148319.
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          18;
        Score 68; DB 2
Pred. No. 6.9;
18; Mismatches
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NHHIRLTISALLT----ALLVTGCVS-TGNVA---MKEQNQQTIEQTIIKGKTNKQEIS 53

10-JUN-1999;
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12-JUN-1999;
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14-MAY-1999
14-JUN-1999
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promoter;
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31-AUG-1999;
31-AUG-1999;
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Best Local
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AAR95910 standard; Protein; 151 AA.
                                                                                                          3 NHHIRLTISALLT----ALLVTGCVS-TGNVA---MKEQNQQTIEQTIIKGKTNKQEIS 53
                                                                                          l Similarity
17; Conserv
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milarity 28.8%;
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990S-0161993
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99US-0160815.
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%; Pred. No. 6.9;
18; Mismatches
                                                                                                                                                                                         DB 21;
6.9;
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                           RESULT
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Best Local Similarity 33.3%;
Matches 14; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae opacity associated proteins OapA (AAR95909) and OapB (AAR95910) are membrane proteins useful as immunogens in vaccines against typable and non-typable H. influenzae infection. They were identified as the products of 2 open reading frames of They gene (AAT27729) isolated from the spontaneous opacity variant an oap gene (AAT27729) isolated from the spontaneous opacity variant H175. Recombinant Oap proteins can be expressed in host cells carrying a vector including an oap gene sequence. Antibodies raised against the proteins are useful for detecting H. influenzae or for passive immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New opacity associated protein of related DNA, vectors, transformed vaccines and for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-239445/24.
N-PSDB; AAT27729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig la-c; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                               ABG02873 standard; Protein; 222 AA
                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                     Novel human diagnostic protein #2864.
                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                               ABG02873;
                                                             WO200175067-A2
                                                                                                  Homo sapiens.
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10; Mismatches
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Note: The sequence data for this patent did not appear in the printed appear in the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
               Human: nootropic: immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                            Human polypeptide
                                                                                                                                                                                      AAM39816
                                                                                                                                                                                                                        AAM39816 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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nes 18; Conserv
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2000US-0649167
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drug
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RESULT 1
AAM41602
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CN ote: The sequence data for this patent did not form part of the printed constraints.
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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14-SEP-2000;
19-OCT-2000;
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Wang
AAM41602;
                                   AAM41602 standard; Protein; 475
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI58972.
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      specification.
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Wang z
Zhou
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2000US-0662191.
2000US-0693036.
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2000US-0598042.
2000US-0620312.
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u P,
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                                                                    11.8%;
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Xu C,
                                                                                                                                                                                                                                                                                                      Score 66;
Pred. No.
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RT;
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Yang
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Zhang J;
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0589042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-065391.
19-CCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                      Query Match 11.8%;
Best Local Similarity 31.6%;
Matches 24; Conservative
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                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide or in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as localised neuropathies and sease, Huntington's disease, amyotrophic Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome of the screening and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic activity, and the screening and shy-Drager Syndrome. Other uses include the lateral sclerosis and the screening and thrombolytic activity, cancer diagnosis and the screening and thrombolytic activity, are screening and throm
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Wang J,
Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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N-PSDB; AAI60758.
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                                                                                                                                                                                                                                                                         Sequence
                                                                                   106
  166
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hte: The sequence data for this patent did not form part of the printed
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                                      FGHTAILAPNRWQEIL 86
                                                                                                                       VSTGNVAMKEQNOOTIEQT----IIKGKTNKQEISS----RFGSADSIS-----FMIVVIK 70
gghtwvkaigrkaeal 181
                                                                                   veagkvaikeshlgstnlthlraivesaenleevvsvlhvfgytdtlgekgtlvvdvvan 165
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                              475 AA;
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Wehrman T, X
, Goodrich R,
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Pred. No. 20;
L1; Mismatches
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Xu C, Xue AJ,
Drmanac RT;
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20;
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Yang Y,
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                                                                                                                                                                                    29;
                                                                                                                                                                                                                          Length 475;
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Zhang J;
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Matches

Local Similarity 32.0 nes 15; Conservative

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Indels

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RESULT 1
AAE04356
           Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200146393-A2
                                                                                                                                  The present invention relates to nucleic acid molecules encoding aspartate kinase useful in cell transformation and transgenic plant production procedures. Nucleic acid encoding aspartate kinase is useful for producing a transgenic plant, by transforming a plant cell with a chimeric gene comprising nucleic acid encoding aspartate kinase with a chimeric gene comprising nucleic acid encoding aspartate kinase operably linked to a regulatory sequence and regenerating a plant from the transformed plant cell. The present sequence is rdrlf.pk005.f20 (FIS) clone Oryza sativa aspartate kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                   Claim 21; Page 56-57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecules encoding aspartate kinase useful in transformation and transgenic plant production procedures \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD08624.
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                                                                                               Sequence
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                                                                                                    281 AA;
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                    11.6%;
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score 64.5; D
Pred. No. 15;
12; Mismatches
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                                                DB 22;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/18a/PCTUS_COMB.pep:*
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US-07-895-200A-1
US-08-458-367-1
PCT-US93-05136-1
US-08-651-999A-3
US-09-247-373B-48
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US-09-247-373B-6
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US-08-148-058A-29
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US-08-477-108A-6	US-08-121-714-6	US-08-840-204-3	US-09-248-588-9	US-09-542-331-2	US-08-411-389-2	US-08-510-284-1	PCT-US94-00198-2	PCT-US94-00198-1	US-07-551-531-2	US-09-476-482-6	US-08-477-451-2	US-09-171-969-9	US-08-564-972-1	US-09-348-817A-4	US-08-948-997-4	US-08-107-042-2	US-08-466-604-29
Sequence 6,	Sequence 6,	Sequence 3,	Sequence 9,	Sequence 2,	Sequence 2,	Sequence 1,	Sequence 2,	Sequence 1,	Sequence 2,	Sequence 6,	Sequence 2,	Sequence 9,	Sequence 1,	Sequence 4,	Sequence 4,	Sequence 2,	Sequence 29
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ALIGNMENTS

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TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-576-3
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US-08-332-576-3
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                                                                           Query Match
Best Local
                                                              Matches
                                                                                                                                                                                                                TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENČE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weiser, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                     LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 19103
                               11 SALLTALLVTGCVSTGNVAMKEQNQQTIE---QTIIKGKTNK 49
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/332,576
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SLIFTALLMTGCVQNANVTTPQAQKMQVEKVDKALQKGEADR
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                                                              Conservative
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Vaccines for
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US-07-895-300A-1
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Best Local (
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                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07895300A patent No. 5279823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,576
APPLICATION NUMBER: 31,1994
FILING DATE: October 31,1994
ATTORNEY,AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-536
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weiser, Jeffrey M. TITLE OF INVENTION: Vaccines
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: Norris
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                             TITLE OF INVENTION: PURIFIED NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SALLTALLVTGCVSTGNVAMKEQNQQTIE---QTIIKGKTNK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                             STREET: 450 FOR CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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                                                                                                     COUNTRY:
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amino acid
GY: linear
                                                                                          94080
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                                                                                                                                                          460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                          360 Kb floppy disk
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Pred. No. 0.31;
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Best Local Similarity 24.2%;
Matches 30; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08458367 Patent No. 5783433
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TELEX: 910/371-7168
TELEX: 910/371-710 NO:
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920608
FILING DATE: 02-Jun-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION UNMBER: 08/409631
FILING DATE: 22-Mar-1995
PRIOR APPLICATION UNMBER: 08/348284
APPLICATION UNMBER: 08/348284
FILING DATE: 30.No. 5783433-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
TOPOLOGY: line
895-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 DQVS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 IA-----LVQEVRDSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERYLEV--YRP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hensley, Max D.
REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 KNLS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 SADSISFMIVVIKFGHTAIL------APNRWQEILSLIIS------FLWVKPYRP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 HHHLRWRGMKLLGALLALAALLOGAVSLKIAAFNIQTFGETKMSNATLVSYIVQILSRYD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NHHIRLTISALLTALLVTGCVSTGNVAMK--EQNQQTIEQTIIKGKTNKQ---EISSRFG 57
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                      APPLICATION NUMBER: US/08/458,367 FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                    94080
                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                          Sliwkowski, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                             PURIFIED
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; Pred. No. 3.4;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 FORMS OF DNase
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PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

07/895300

08/116186

FILING DATE: APPLICATION NUMBER:

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US-08-458-367-1
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TELEPHONE: 415/925-3562
TELEFAX: 415/925-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Applicati
GENERAL INFORMATION:
APPLICANT: Genent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PURIFIED FORMS OF DNase NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/8: FILING DATE: 08-Jun-1992 ATTORNEY/AGENT INFORMATION: NAME: Johnston, Sean A.
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/No TO RRENT NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 DQVS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 KNLS 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P0747C4
                                                                                    NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 747PCT
                                                                                                                                                                                                               APPLICATION NUMBER: PFILING DATE: 19930528 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 SADSISFMIVVIKFGHTAIL------APNRWQEILSLIIS------FLWVKPYRP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 HHHLRMRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLVSYIVQILSRYD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                               94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application PC/TUS9305136
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                                                                                                                                                                                                                                                                                                                                                                                                USA
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24.2%; Pred. No. 3.
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; HYPOTHETICAL: ; FRAGMENT TYPE: US-08-651-999A-3
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US-08-651-999A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LENGTH: 346 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US93-05136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.2
Matches 30; Conservative
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                                                                                                                                                             TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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LENGTH: 346 amino acid
                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stefan Somlo and Toshio MCTITLE OF INVENTION: POLYCYSTIC KIDNEY
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/65
FILING DATE: MAY 23, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
                                                                 MOLECULE TYPE
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                  DESCRIPTION:
                                                                                 TOPOLOGY:
                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                  TELEFAX:
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                                                                                                                              399 amino acids
                                                                                                                                                                                                (212) 286-0854 or 286-0082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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/ENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC COMPATIBLE
                                                                                 linear
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                                                                                                                                                                                                                 (212)
               internal fragment
                                              peptide
                                                                                               single
                                                                                                                                                                                                                   697-5995
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24.28;
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Pred. No. 3.4;
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Query Match 10.7 Best Local Similarity 23.9 Matches 26; Conservative

10.7%; Score 59.5; I 23.9%; Pred. No. 14; tive 14; Mismatches

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Length 399;

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Patent No. 6228591
GENERAL INFORMATION:
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 D,
                                                                                                                       Query Match
Best Local Similarity
Matches 26; Conserv
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APPLICATION NUMBER: 08/651,99
FILING DATE: MAY 23, 1996
ATTORNEY/AGENT INFORMATION:

NAME: ELIZABETH A. BOGOSIAN

REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                         DESCRIPTION:
HYPOTHETICAL:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ALLTALLVTGCVSTGNVANKEQNQQTIEQ-----TIIKGKTNKQEISSRFGSADS----- 61
                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                 62
                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHTRAVIIEFSAYNAQINYFSVVQLLVEIPKSGIYLPNSWVESVRLIKS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLATALLASWYDGNPAYGMRAYMNDKVSRSMGIGTIRQVRTKKSEIITLFNKLDSERWID 138
DHTRAVIIEFSAYNAQINYFSVVQLLVEIPKSGIYLPNSWVESVRLIKS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10016
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                                                                                                                                                                                                                                                                                                                     amino acid
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VENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
VENTION: AND USES THEREOF
EQUENCES: 12
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                                                                                                                                                                                                                                                                                  ESS: single
linear
                                                                                                                              Conservative
                                                                                                                                                                                                                            internal fragment
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                                                                                                                                               10.7%;
23.9%;
                                 -ISFMIVV---IKFGHTAILAPNRWQEILSLIIS 91
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                                                                                                                            ; Score 59.5; DB 4; Length 399;
; pred. No. 14;
14; Mismatches 40; Indels 2
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                                                                                                                                        29;
                                                                                                                                        Gaps
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RESULT

DeMuth, Donald R

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SOFTWARE: MICROSOFT
SEQ ID NO 48
LENGTH: 229
TYPE: PRT
ORGANISM: SOYBEAN
US-09-247-373B-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-247-373B-48
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; Sequence 2, Application US/09238481
; Patent No. 6110704
                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus aureus US-09-238-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                               RESULT 10
US-08-374-843B-6
; Sequence 6, Application US/08374843B
; Patent No. 5726016
; Patent No. 5726016
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APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10192
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBBAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
GENERAL INFORMATION:
APPLICANT: DeMuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 WEEVGSMQIIDPLKFPATTEWITNFLSHPLIKDSLPPRDKMLVYYHNRK 216
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                                                                                                                                                                                                                                                                  y Match 10.5%;
Local Similarity 23.1%;
les 27; Conservative 1
                                                                                                                                 47 TNKOEISSREGSADSISEMI--VVIKEGHTAILAPN-----RWQEIL 86
                                                                                                                                                                                                   1 MKMTKSALVTG-----ASRGIGRSIALQLAEEGYNVAVNYAGSKEKAEAVVEEIKAKG-
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25.7%; Pred. No. 8.8;
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                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                                                                                                            Score 58.5; Di
Pred. No. 9.7;
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                                                                                                                                                                                                                                                                                                                  Length 246;
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OPERATING SYSTEM:

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US-08-374-843B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Leary, Kathryn Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEPHONE: (215) 567-2991
TELEFA: (215) 567-2991
TELEFA: 831-494
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        Patent No. 5726016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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TOPOLOGY: 1'
(OLECULF '
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                 APPLICANT: Demuth, Donald I APPLICANT: Lally, Edward T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/00 FILING DATE: 18-JAN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF DISEASES ASSOCIATED WITH ACTINOBACILLUS
TITLE OF INVENTION: ACTINOMYCETEMCOMITANS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 QQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVIKF--GHTAILAPNRWQEILSLIISF 92
                                                                                                    STATE:
                                                                                                                  CITY: Philadelphia
                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 LWVKPYRPKNLSFY 106
                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSTFNDGMLEGEAAKQEVSRTLRSSALLVASAIVIHFKSNFTNLL-----ILSQITQY 112
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                                                               19103-2398
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                                                                                                Pennsylvania
                                                                                                                                                                                                                                                                                                                                           Application US/08374843B
                                                                                                                                   E: PANITCH SCHWARZE JACOBS & NADEL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/374,843B
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RESULT 12
US-08-905-420-6
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Patent No.
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TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DeMuth, Donald R.
APPLICANT: Laily, Edward T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF DISEASES ASSOCIATED WITH ACTINOBACILLUS
TITLE OF INVENTION: ACTINOMYCETEMCOMITANS INFECTION
             NAME: Leary, Kathryn Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596-7 (F-1080)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0)
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596-7 (F-1080)
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                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19103-2398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6, Application US/08905420
5. 5861255
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(215)567-2991
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n Release #1.0,
                                                                                                                                                   US 08/374,843
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TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

6:

LENGTH:

1: 150 amino acids amino acid

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-905-420-6
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Best Local Si
Matches 20
                                                         US-08-905-420-10
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Query Match
Best Local Similarity
                                                                                                                            TELEFAX: (215)567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acid
                                                                                                                                                                                            FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
ANAME: Leary, Kathryn Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215)567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DeMuth, Donald R.
APPLICANT: Lally, Edward T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF DISEASES ASSOCIATED WITH ACTINOBACILLUS
TITLE OF INVENTION: ACTINOMYCETEMCOMITANS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: YSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                            TYPE: amino acid
                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: PANITCH SCHWARZE JACOBS & NADEL, P.C. 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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linear
                                                                                                                                   150 amino acids
                                                                                                     linear
                                                                                   protein
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      10.2%;
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                                                                                                                                                                      10:
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      Score 57; DB 2; pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                          Length 150;
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TELEX: N/A
TELEX
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                                                                                                RESULT 15
US-08-505-307-19
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; sequence 19, Application US/08505307 ; patent No. 6083691 ; GENERAL INFORMATION:
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APPLICANT: Deretic, Vojo
APPLICANT: Martin, Daniel W.
APPLICANT: Martin, Daniel W.
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCCOLDY IN
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 19
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hodgins, Daniel S. 1026
REGISTRATION NUMBER: 31.026
REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19930212
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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STATE: Texas
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ZIP: 77210
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FILING DATE: 19930212
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                                                                                                                                                                                                                                                                                                        91 SFL------WVKPYR 99
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les 19; Conserv
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23.2%;
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CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/017,114
APPLICATION NUMBER: US 08/017,114
FILING DATE: 12-FEB-193
ATTORNEY/AGENT INFORMATION:
NAME: HODGINS, Daniel S.
REGISTRATION UMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK:231
TELECOMMUNICATION: TORNATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 anino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-505-307-19
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Search completed: July 30, 2002, 15:38:55 Job time: 184 sec
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APPLICANT: Martin, Daniel W.
APPLICANT: MARTIN: DETECTION OF CONVERSION TO MUCOIDY IN
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/505,307 FILING DATE: 24.007-1995
                                                                                                                                                                                                                        31 KEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVIKFGHTAILAPNRWQEILSLII 90 :||:||:|| :|| :|| :|| :||
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STATE: TX
                                                                                                            39 RFVHDAQEAQDVAQEAFIKAYR 60
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Title:
Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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1: pir1:*
2: pir2:*
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hypothetical lipoprotein [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli C;Pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: B91067 R;Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: B91067 A;Accession: B91067 A;Status: preliminary A;Molecule type: DNA A;Rosidus: 1-131 <HAY> A;Rosidus: 1-131 <HAY> A;Cross-references: GB:BA000007; PIDN:BAB36929.1; PID:g13362977; GSPDB:GN00154 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: B91067

Ω 멍 Š 뮹 Query Match Best Local Matches 79 75 19 17 LLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVIKFGHT-------AILAPNRWQEILSLIISF LTLAGCSSVGNQSLKNETQESVKTKIVKGKTTKQDVLASFGEPDSRSLIDGEEQWSYTMY 78 NSQSKATSFIPVVGLLAGGADSQTKSLTVSF . Similarity 27; Conserv Conservative 21.1%; Score 117.5; DB 2 29.7%; Pred. No. 4.3e-05; Live 19; Mismatches 30 92 DB 2; 30; Length Indels 131; 15; Gaps 74 ۲

Son, S.; H

cation efflux system protein [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: H95216
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95216 Morris

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-299 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75929.1; PID:g14973359; GSPDB:GN00164; TIGR:

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A; Experimental & C; Genetics: A; Gene: SP1857
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hypothetical protein czcD [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Cpate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: F98080
C;Accession: F98080
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.
R; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
P.; Sun, P.M.; Winkler, M.E.
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
J. Racteriol. 183, 5709-5717, 2001
A;Accession: F98080
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F98080
A;Status: preliminary
A;Molecule type: DNA
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                                               iron(III) dicitrate-binding periplasmic protein [imported] - Anabaena sp. (strain C;species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AH2128 R;Kaneko, T; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Ir R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, M.; Yasuda, M.; Tab. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tab. DNA Res. 8, 205-213, 2001
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A;Title:.Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Molecule type: DNA
A;Residues: 1-328 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74282.1; PID:917131675; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein NMA0510 [imported] - Neisseria meningitidis (strain Z2491 C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 *sequence_revision 05-May-2000 *text_change 02-Feb-2001 C;Date: 05-May-2000 *sequence_revision 05-May-2000 *text_change 02-Feb-2001 C;Accession: B81969 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quall, M.A.; Ra
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A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A;Reference number: A81775; MUID:20222556
A;Accession: B81969
                                                                                  hypothetical protein slll158 - Synechocystis sp. (strain PCC 6803)
C. Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Accession: S74868
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, R; Kocession: S7486
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Wada, T.; Watanabe, A.; Yamada, M.; Yaso, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaso, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasa, June Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
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Nature 404, 502-506, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-112 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
A; Reference number: S74322;
A; Accession: S74868
A; Status: preliminary
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          64 TVGK 67
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milarity 31.4%;
Conservative 14
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                                                         MUID:97061201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
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C:Species: Bacillus subtilis
C:Conte: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Conte: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Conte: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Accession: C70078
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteteile
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: C70078
A;Status Tracilminary Duclaic anid source of the Gram-positive bacterium Bacillus subtilis.
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C70078
hypothetical protein yxiP - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C;Date: 05-Dec-1997 #text_change 28
                                                                                                                                                              RESULT 8
749962
749962
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-un-2000 #sequence_revision 02-un-2000 #text_change 02-Jun-2000
C;Accession: T49962
R;Bevan, M; Murphy, G; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.;
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A; Residues: 1-138 < KAN>
A; Residues: 1-138 < KAN>
A; Cross*references: EMBL.D90909; GB:AB001339; NID:g1652844; PIDN:BAA17829.1;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
C; Superfamily: Synechocystis hypothetical protein sill1158
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C;Superfamily: Bacillus subtilis hypothetical protein yx1P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-226 <KUN>
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                                            A; Reference number: Z24493
A; Accession: T49962
                                                                                                                               R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 5.2;
3; Mismatches 16;
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Pred. No. 2.4;
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                                                                                                                                                              A;Title: The genome sequence of Rickettsia A;Reference number: A71630; MUID:99039499 A;Accession: E71663
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T40178
                                                                                                                                                                                                                                                                                          C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: E71663 R;Andersson, S.C.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-export membrane protein secd (secD) RP586 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
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                                            A; Molecule type: DNA
A; Residues: 1-518 <A
                                                                                                                       A; Status: preliminary; nucleic acid
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A;Cross-references: GB:AJ235272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 VSLLKKG---
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<AND>

GB:AJ235269; NID:g3861033; PIDN:CAA15031.1; PID:g386

sequence not shown; translation not shown

prowazekii

and

the origin of mitochondria.

WONIGSLVIKSTMGKPYR 214

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Query Match
Best Local Similarity
"~+~hes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60s ribosomal protein L10 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                       A;Map position: 2
A;Introns: 130/1
C;Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: Z97992; PIDN: CAB10813.1; A; Experimental source: strain 972h-; cosmid c30D10
                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z21910
A; Accession: T40178
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R;Wood, V.; Rajandream, M.A.;
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A; Introns: 200/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-568 <BEV>
                                                                                                                                                                                                                                   A; Gene: rpl10a-2;
                                                                                                                                                                                                                                                         C; Genetics:
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                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                            R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ATSP: F8M21.160
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150 VKSTIKFQLKKVLCLG-VAVGHVDMAE---
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                                  6 IRLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFM 65
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                                                                           Conservative
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                                                                                            12.6%;
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Pred. No. 16;
L4; Mismatches
                                                                                            Score 70.5; D
Pred. No. 6.3;
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                                                                           Mismatches
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bruary 1998
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                                                                                                              Length
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G94145
Gypothetical protein H10230 - Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
R;File: Gelischmann, Z.L.; Mrither, Y.L.; File: L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.
C;Cotence 269, 496-512, 1995
A;Rathors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Tulte: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Rathors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Rathors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Accession: G64145
A;Accession: G64145
A;Accession: G64145
A;Accession: G64145
A;Cross-references: GB:U32709; GB:L42033; NID:g1573190; pIDN:AAC21899.1; pID:g1573194; TA;Accession: G64145
A;Rote: Dest homolog was a hypothetical protein from Escherichia coll
A;Rote: Dest homolog was a hypothetical protein from Escherichia coll
A;Rote: Dest homolog was a hypothetical protein from Escherichia coll
A;Rote: Dest homolog was a hypothetical protein from Escherichia coll
A;Rote: Dest homolog was a hypothetical protein from Escherichia coll
A;Rote: Dest homolog was a hypothetical protein from Escherichia coll
A;Rote: Dest homology coll
B;Rotenzae Rd.
A;Rotenzae Rd.
A;Rote
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C; Genetics:
A; Gene: secD; RP586
C; Superfamily: protein
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hypothetical protein at2g37660 [imported] - Arabidopsis thaliana hypothetical protein F13M22.16
N;Alternate names: hypothetical protein F13M22.16
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T02532; E84795
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Bounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; Ketchum, R.C.; Crosby, M.L.; Brandon, R.C.;
R;Rounsley, S.D.; 
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3; Mismatches
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Pred. No. 12;
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; T
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: E84795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euss, D.; Nierman, W.C.; V. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2
A;Introns: 89/1; 179/3; 192/1; 236/3; 257/2; 298/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE002093; NID:g3236248; PIDN:AAC23636.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-337 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: At2g37660; F13M22.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    R; Wilson, R.; Favello, A.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid F21F8.
A; Reference number: Z20618
A; Recession: T29418
A; Accession: T29418
A; Molecule type: DNA
A; Molecule type: DNA
A; Hoseidues: 1-330 < NIL
A; Residues: 1-330 < NIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F21F8.11 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Species: Caenorhabditis elegans 15-Oct-1999 #text_change 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U97000; PIDN:AAC47997.1; GSPDB:GN00023; A;Experimental source: strain Bristol N2; clone F21F8
                                                                                                                                                                                                                                                                                                              A; Map position:
A; Introns: 16/1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFGSADSISFMIVVIKFGHTAILAPNRWQEILSLIISFLWVKPYRP----
                                                                    CTKLEGKVIKDYGGTFIWSVSWQGYIVSAAFLGGFIFSYPAGVLVDRFSARHILSVAILM
                                                                                                                                               HIGLSLSCMCNSTAV-ALMNTNNATLVEGTESTILMSILENKTSE---SQELGGGDDGES 99
                                                                                                                                                                                HIRLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
36; Conserv
                                     LWVKPYRPKNLSFYLTAK 110
                                                                                                                                                                                                                                                                                                                    16/1;
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                                                                                                                                                                                                                                                                                                                64/2; 112/3; 344/3; 417/1;
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                                                                                                                                                                                                                                             12.4%; Score 69; DB 21.7%; Pred. No. 24;
                                                                                                             -SISFMIVVIK------FGHTAILAPNRW--QEILSLIISF 92
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Pred. No. 13;
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L.; Tallon,
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RESULT 15
E71179
hypothetical protein PH1714 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: E71179
C;Accession: E71179
C;Accession: E71179
C;Accession: E71179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Accession: E71179
Search completed: July 30, 2002, 15:39:18 Job time: 127 sec
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C:Superfamily: secretion protein xcpS
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A;Residues: 1-391 <ARN>
A;Cross-references: GB:AE001327; GB:AE001273; NID:g3328999; PIDN:AAC68172.1; PID:g332901
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: C71499
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, R;Stephens, R.S.; Fan, S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, R;Celence 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Reference number: A71570; MUID:99000809
A;Accession: C71499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable gen. secretion protein F - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30828.1; PID:g3258145
A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-405 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.3%; Score 68.5; I Best Local Similarity 22.5%; Pred. No. 20; Matches 27; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.3
Best Local Similarity 21.7
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                     6 IRLTISALLTALLYTGCVSTGNVAMKEQNQOTIEQTIIKGKTNKQEISSRFGSADSISF- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMI----- 66
                                                                                                                                              55 DMAYLGAERAKKELGVKIEY-----MTPKSKEDMVPLLEQLAKSKEYDLLVLVGFLWTTP
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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OAPB_HAEIN
RY5A_HUMAN
TRPD_SULSO
SECV_CYAPA
V406_MYCPN
RPAL_SULSO
SECV_CYAPA
V406_MYCPN
RPAL_SULSO
MY5A_RAT
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MY5A_RAT
DDOL_NPVAC
PR22_YEAST
POUL_PESMY
ORC4_MOUSE
YMDB_YEAST
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p42307 bacillus su
014363 schizosacch
092cw# rickettsia
p44585 haemophilus
080934 arabidopsis
059403 pyrococcus
p44416 haemophilus
074836 schizosacch
p71496 mycoplasma
000157 ictalurid h
09y411 homo sapien
p50384 sulfolobus
p25014 cyanophora
050325 mycoplasma
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P56862 aspergillus	MET3_ASPTE	-	568	10.7	59.5	G
P40407 bacillus su	YBBC_BACSU	دبر	414	10.7	59.5	4
Q9ubq6 homo sapien	EXL2_HUMAN	-	330	10.7	59.5	ω
083466 treponema p	SYI_TREPA	۲	1091	10.8	60	N
P32349 saccharomyc	RPC3_YEAST	ب	654	10.8	60	_
079437 oryctolagus	NU5M_RABIT	_	603	10.8	60	0
P21131 streptococc	TACY_STRPY	ب	571	10.8	60	Ø
P10550 sonchus yel	NCAP_SYNV	_	475	10.8	60	æ
P44132 haemophilus	YC36_HAEIN	ب	367	10.8	60	7
054873 cricetulus	MCA1_CRIGR	ب	359	10.8	60	σ
Q9wy63 thermotoga	FLIG_THEMA	_	335	10.8	60	G
P27291 escherichia	OSMY_ECOLI	_	201	10.8	60.5	4

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60s ribosomal protein L1-A (L10A).
RPILA OR SPBC30D10.18C.
RPILA OR SPBC30D10.18C.
Schlzosaccharomyces pombe (Fission yeast).
Schlzosaccharomycetales; Schlzosaccharomycetes;
Eukaryota; Fungi; Ascomycota; Schlzosaccharomycetaceae;
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Q9ZCW8;
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ProDom; PD001314; Ribosomal_L1; 2.
PROSITE; PS01199; RIBOSOMAL_L1; 1.
Ribosomal protein; Multigene family.
SEQUENCE 216 AA; 23884 MW; 676EF
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SEQUENCE FROM N.A.

STRAIN-MADRID E;

MEDLINE-99039499; pubMed-9823893;

Andersson S.G.E., Zomorodipour A.

Sicheritz-Ponten T., Alsmark U.C.
                                                                                                     Bacteria; Proteobacteria; alpi
Rickettsiaceae; Rickettsieae;
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                                                                                                                                                              Protein-export membrane
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    Zomorodipour A., Andersson J.
I., Alsmark U.C.M., Podowski R
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eae; Rickettsia.
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WHICH COMPRISE SECA, SECB, SECD, SEC
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pfam; pF02355; SecD_SecF; 1.
protein transport; Translocation; Transmembrane;
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                  SEQUENCE FROM N.A.

STRAIN-RD / KW20 / ATCC 51907;

STRAIN-RD / KW20 / ATCC 51907;

STRAIN-RD / KW20 / ATCC 51907;

STRAIN-PS350630; PubMed=7542800;

MEDLIND-95350630; PubMed=7542800;

MELIND-95350630; PubMed=7542800;

MELIND-95350630; PubMed=7542800;

Melind-953600; PubMed=7542800;

Melind-953600; PubMed=7542800;

Melind-953600; PubMed=7542800;

Melind-953600; PubMed=7542800;

Melind-953600; PubMed=7542800;

Melind-10, Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Wenter J.C.;

Wenter J.C.;
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NLPI OR HI0230.
                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
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Whole-genome random sequencing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSA-----DS
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31; Conservative
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518 AA;
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32, Last sequence up
40, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor
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               assembly of Haemophilus
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6.9;
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Best Local
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16-OCT-2001 (Rel. 40, La
16-OCT-2001 (Rel. 40, La
16-OCT-2001 (Rel. 40, La
Protein At2937520, Chior
AT2637520 OR F13M22-16.
                                                                                    Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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080934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                    "Sequence and analysis of chromosome thaliana.";
                                                                            Venter J.C.;
                                                                                                                                                                                                                             STRAIN-CV. COLUMBIA;
MEDLINE-20083487; PubMed-10617197;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702
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FUNCTION: MAY BE INVOLVED IN CELL
SUBCELLULAR LOCATION: Attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 3 TPR REPEATS
SUBCELLULAR LOCATION: Chloroplast (Potential)
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                    402:761-768(1999)
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40, Last annotation updat
chloroplast precursor.
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27.1%;
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Pred. No. 4.5;
3; Mismatches
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N-ACYL DIGLYCERIDE.
TPR 1.
TPR 2.
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Best Local Similarity
Matches 36; Conserv
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15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y. Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Oshakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohf Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                             This
                                                                                                                                                                                                                                                            "Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus DNA Res. 5:55-76(1998).
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O59403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast;
                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98344137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; NCBI_TaxID-53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus horikoshii.
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EMBL; AP000007;
                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
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                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                        (Potential).
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BAA30828.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed-9679194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36085 MW;
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PROTEIN AT2G37520.
; 748838ECB4BA07CD CRC64
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Pred. No. 4.9;
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                                                      . Usage by and for http://www.isb-sib.
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IPR003760;

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ID OAPB.H
AC P44416
AC OAPB OC OAPB
OS OAPB OC OAPB
OC Haemop
OC Haemop
OC Haemop
OC Haemop
AC STRAIT
RX MEDLII
RA WEIse;
RA WEISE;
RA WEISE;
RA F1001.]
RY THAEMO;
RY THAEMO;
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RX MEDLII

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Matches 27
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SIGNAL 1 20 PROBABLE.
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                                                                                                                                                                                                                                                                                                                                                                            STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Stylon G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu E.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hebblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weiser J.N., Chong S.T., Greenberg D., Fong W.;
"Identification and characterization of a cell envelope protein and characterization of a cell envelope protein and passity influenzae contributing to phase variation in colony opacity and nasopharyngeal colonization.";
Mol. Microbiol. 17:555-564(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Opacity associated OAPB OR HI0331.
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01-NOV-1995 (Rel. 32,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P44416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96100454; PubMed-8559074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
     EMBL; U17037;
EMBL; U32718;
TIGR; H10331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                 modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                         influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
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                                     AAA56762.1; -.
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                                AAC21993.1;
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Pred. No. 7.5;
17; Mismatches
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N-ACYL DIGLYCERIDE (PROBABLE).
, 605D545798B6A5A2 CRC64;
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                                                                                                                                            . Usage by and for commercial http://www.isb-sib.ch/announce/
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CONFLICT 133
SEQUENCE 134 AA;
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Bukaryota; Fungi; Ascomycota; Schizosaccha
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NCBI_TaxID=4896;
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probom; pB001314; Ribosomal_L1; 2.
proSITE; pS01199; RIBOSOMAL_L1; 1.
Ribosomal protein; Multigene family,
SEQUENCE 216 AA; 23917 MW; D99F6
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pred. No. 4.9;
18; Mismatches
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Matches 15
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Q00157;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics in the European Bioinformatics in the earn no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                               Ictalurid herpesvirus 1 (Channe Viruses; dsDNA viruses, no RNA unclassified Herpesviridae. NCBI_TaxID-10401;
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                                                                                                                                                                    "Channel catfish virus: a new type Virology 186:9-14(1992).
                                                                                                                                                                                                                   Davison A.J.;
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Pfam; PF00472; RF-1; 1.
PROSITE; PS00745; RF_PROK_I; 1.
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FUNCTION: PEPTIDE CHAIN RELEASE FACTOR 1 DO FUNCTION: PEPTIDE OF TRANSLATION IN RESPONSE TO THE PEPTIDE CODONS UAG AND UAA (BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULARITY: BELONGS TO THE PROKARYOTIC AND CARROLLE CONTROLLE C
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27343 / KID;
86911; PubMed-8635731;
Worl H., C
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MY5A_HUMAN
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Best Local
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Pastural E.,
Jabado N., S
Nat. Genet.
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                                                                                                         Engle L.J., Kennett R.H.; "Cloning, analysis, and chromosomal localization the human homologue to the mouse dilute gene."; Genomics 19:407-416(1994).
                                                                                                                                                                                                                                                        Pastural E., Barrat F.J., Dufourcq-Lagelouse R., Certain S., Sa
Jabado N., Seger R., Griscelli C., Fischer A., de Saint Basile
"Griscelli disease maps to chromosome 15q21 and is associated w
mutations in the myosin Va gene.";
Nat. Genet. 16:289-292(1997).
                                                                                                                                                    MEDLINE-94245227; F
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), F
MEDLINE=97351514; PubMed=9207796;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 5
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                    Jenkins N.A.; "Cloning and regional assignment of the human (MYH12) gene to chromosome band 15q21.";
                                                      Moore K.J., Testa
                                                               MEDLINE-95136715;
                                                                                       SEQUENCE OF 1061-1498 FROM N.A.
                                                                                                                                                                             SEQUENCE OF 638-1477 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                               myosin.
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21; Conservative
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                                                                                                                                                                                                   ., Barrat F.J., Dufourcq-Lagelouse R Seger R., Griscelli C., Fischer A., 23:373-373(1999).
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599 AA; 67476
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          Cenet. 69:5
                                                   PubMed=7835087;
J.R., Francke U
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33.9%;
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Catarrhini; Hominidae
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de s
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pfam; pF01843; DIL; 1.
pfam; pF00612; IQ; 6.
pfam; pF00063; myosin_head; 1.
pfam; pF00063; myosin_headvv.
pRINTS; pR00193; mYoSin_head; 1.
proDom; pD000355; myosin_head; 1.
proDom; pD003376; DIL; 1.
SMART; SM00015; IQ; 6.
SMART; SM00042; MYSS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1358-1460 FROM N.A. (ISOFORM 3). Edgar A.J., Bennett J.P.; ranshibition of dendrite formation in melanocytes transic transfected with antisense DNA to myosin V."; submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin-V is a processive actin-based motor.")
Nature 400:590-593(1999).
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HSSP;
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InterPro; IPR000048;
InterPro; IPR001609;
                                                                                                          Myosin;
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FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGE FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGE STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAMENT. ANY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MAY BE REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE PORMATION.

SUBJURIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE SUBJURIT: MAY BE A HOMODIMER, WHICH
                                                                                                                                                                                                                                                                                  ;; U90942; AAD00702.1; -.
;; Y07759; CAA69035.1; -.
;; Y07759; CAA69036.1; -.
;; Z22957; CAA80533.1; -.
;; S74799; AAB33211.1; -.
;; AF055459; AAC14188.1; -.
                                                                                                 coil;
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MEDLINE-21332296; PubMed-11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., Awayez M.J., Chan-Weiher C., Gordon P.M.K., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., De Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pen Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Wedina N., Pen Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Colstrup Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolbus solfataric" Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Anthranilate phosphoribosyltransferase (EC 2.
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Tutino M.L., Cubellis M., Sannia G.,
"The tryptophan operon in Sulfolobus
Submitted (JUL-1995) to the EMBL/GenE
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Archaea; Crenarchaeota;
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                                                                                   CHARACTERIZATION, AND CRYSTALLIZATION.
CHARACTERIZATION, AND CRYSTALLIZATION.
CHARACTERIZATION, PROBAGAIL 1298741;
MEDLINE=21195237; PubMed=11298741;
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner Ivens A., Mayans O., Szadkowski H., Wilmanns M., 
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    19 VTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSREGSADSISE
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17; Conserv
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nilarity 37.0%;
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*a: 215419 '
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F -> L (IN REF. 1).

MISSING (IN REF. 4).
E -> G (IN REF. 1).
H -> R (IN REF. 1).
V -> L (IN REF. 5).
E -> Q (IN REF. 5).
D -> E (IN REF. 5).
NIPRKEKDFOGML -> SVI
4).
C -> N (IN REF. 5).
K -> N (IN REF. 5).
K -> N (IN REF. 5).
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No. 72;
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solfataricus
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Matches
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EMBL; AE006710; AAK41173.1; -.
InterPro; IPR000312; Glycos_transf_3.
Pfam; PF00591; Glycos_transf_3; 1.
Pfam; PF02885; Glycos_transf_3; 1.
ProDom; PD001864; Glycos_transf_3; 1.
Tryptophan blosynthesis; Transferase; G.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-91117189; P Michalowski C.B., P The cyanelle S10 s
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P25014;
01-MAR-1992
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-LB555 / PRINGSHEIM;
Stircwalt V.L., Michalowski C.B., Loeffelhardt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 345 AA;
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NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preprotein
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16-OCT-2001
         STRAIN-LB555 / PRINGSHEIM;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B.,
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spa
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant i
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                       Bryant D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyanelle
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                                                                                                                                                                            "Nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
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                                                                                                                                                                                                                                                                                                                                                             ; PubMed=2126059;
, Pfanzagl B., Loe
O spc ribosomal pr
                                                                                                                                                      Rep.
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                                                                                                                                                   of the cyanelle DNA 13:327-332(1995).
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Last annotation update)
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Pred. No. 13;
21; Mismatches
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L protein gene operon
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ישאגו C.B., Annarella
Newmann-Spallart C.,
J., Bryant D.A.;
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                                                                                                                                                                            Cyanophora
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ANTCC 29:42 / M129;

C STRAIN-96177562; PubMed-8604303;

K MEDLINE-96177562; PubMed-8604303;

RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;

RT "Sequence analysis of 56 kb from the genome of the bac

RT "Sequence analysis of 56 kb from the genome of the bac

RT Mycoplasma pneumoniae comprising the dnaA region, the

cluster of ribosomal protein genes.";

cluster of ribosomal protein genes.";
                             CRETTARA KRETTTARA KRETTARA KR
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                          Nucleic
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PROSITE; PS00755; SECY_1; 1.
PROSITE; PS00756; SECY_2; 1.
Protein transport; Transmembrane; Cyanelle; Translocation.
Protein transport; Transmembrane; B736219112EBFCOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-AFTCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasmataceae;
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacilli
Mycoplasmataceae; Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete sequence of the cyanelle genome of the genetic complexity of a primitive plastid."; (In) Schenk H.E.A., Herrmann R., Jeon K.W., Muell Schwemmler W. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q50325;
01-NOV-1997
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                                                                           pneumoniae.
                                                                                                                                 Herrmann
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                                                                                                "Complete sequence
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CY.
SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                          SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAFIQSIVISWIWIRPY-ALNWDFFLGLK 188
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12; Conser
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Res. 24:4420-4445(1177)
AR LOCATION: Integral membrane
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                                                                                                   analysis
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annotation update)
homolog (C12_orf157L).
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RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA De Moors A., Erauso G., Fletcher C., Kozera C.J., Medina N., Peng X.,

RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Tolstrup N.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Charlebois R.L., Bagan M.A., Sensen C.W., Yan der Oost J.;

RA GARTETT R.A., Ragan M.A., Sensen C.W., Yan der Oost J.;

RA GARTETT R.A., Radad Sci. U.S.A. 98:7835-7840(2001).

L PROC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

L PROC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

L PROC. Natl. DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

C. OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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TRANSMEM 81 101 POTENTIAL.
TRANSMEM 112 132 POTENTIAL.
SEQUENCE 157 AA; 18291 MW; 7D9097A405DAD3C4 CRC64;
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EMBL; AE000024; AAG34742.1;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Created)
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                                                                                         (RNA)(N).
COPACTOR: ZINC (By similarity).
SIMILARITY: THE COMBINED A'+A" SUBUNITS
SUBUNITS OF EUKARYOTIC RNA POLYMERASES I
EUBACTERIAL BETA' SUBUNIT.
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CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Search completed: July 30, 2002, 15:42:00 Job time: 184 sec

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                                                                                                                                                                                                             pfam; pF00623; RNA_pol_A; 1.
Transferase; DNA-directed RNA polymerase;
Zinc-finger; Complete proteome.
ZN_FING 58 101 C4-TYPE (POTI ZN_FING 58 0) AA; 99674 MW; 5C8AEZ0EFC
                                                                                                                                                                                                                                                                                        EMBL; AE006659; AAK40566.1; -.
Interpro; IPR000722; RNA_pol_A.
                                                                                                                                                                                                           SEQUENCE
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                                                               TVKTTLL----TKEEAQQILGVAD-----VKIDLGEPAILAPREYYTGKQVISAFL---
   ---PKDFNFH 563
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                                                                                                                                Similarity 30.0
21; Conservative
                                                                                                                                11.5%; Score 64; DB 30.0%; Pred. No. 52; tive 11; Mismatches
                                                                                                                                                                                                               C4-TYPE (POTENTIAL).; 5C8AE20EFC71DE25 CRC64;
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Listing first 45 summaries
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777.741 Million cell updates/sec
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
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11: sp_rodent::
12: sp_virus:*
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Copyright (c) 1993 - 2000 Comp
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sp_virus:*
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Q97nz2 streptococc
Q9pum2 xenopus lae
Q915c3 lactobacill
Q9jw76 neisseria m
P73777 synechocyst
Q91xf5 arabidopsis
Q91u91 human immun
Q901a9 human immun
Q901a9 human immun
Q901a9 caenorhabdi
Q9kzz5 streptomyce
Q00947 tetrahymena
Q84574 chlamydia t
Q77772 oryctolagus
Q94b61 arabidopsis
P87977 human immun
Q9ce58 lactococcus
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ALIGNMENTS

Query Match 14.0%; Score 78; DB 16; Length 299; Best Local Similarity 28.3%; Pred. No. 2.6; Matches 36; Conservative 18; Mismatches 39; Indels 34;	RESULT 1 (297NZ2; PRELIMINARY; PRT; 299 AA. AC 097NZ2; DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) DT 01-OCT-2001 (TREMBLrel. 19, Last annotation update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE CATION EFFLUX SYSTEM PROTEIN. GN SP1857. OS Streptococcus pneumoniae. OC Streptococcus. OC Streptococcus. OX NCBI_TAXID=1313; RN [1] RP SEQUENCE FROM N.A. STRAIN=TIGR4; RX MEDLINE=21357209; PubMed=11463916; RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., RA Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J., RA HOLTINE=21357209; PubMed=11463916; RA HOLTINE-21357209; PubMed=11463
; 34; Gaps 6	occaceae; D., J.D., J.D., Hickey E.K., M.; COCCUS

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                       Query Match
Best Local S
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Pfam; PF000629; MAM; 1.

Pfam; PF00102; Y_phosphatase; 1.

Pfam; PF00102; Y_phosphatase; 1.

Pfam; PF00102; Y_phosphatase; 1.

PRINTS; PR00100; MAXDOMAIN;

PRINTS; PR00700; PRTYPHPHTASE.

SMART; SM00060; FN3; 3.

SMART; SM00137; MAM; 1.

SMART; SM00137; MAM; 1.

SMART; SM00134; PTPC; 1.

SMART; SM00134; PTPC; 1.

SMART; SM00137; MAM; 1.

SMART; 
Matches
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR PROTEIN TYROSINE PHOSPHATASE RHO PRECURSOR (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
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"Xenopus laevis receptor protein tyrosine phosphatase rho.";

submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

submitted (JUL-1999) to the EMBL/GenBank/DBBJ databases.

1- SIMILARITY: CONTAINS 1 MAM DOMAIN.

EMBL; AR173857; AAD50295.1;

EMBL; AR173857; ARD50295.1;

HSSP; P28827; 1RPM.
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MEDILINE-20193505; PubMed-10727868;
MEDILINE-20193505; PubMed-10727868;
Johnson K.G., Holt C.E.;
Johnson K.G., Holt C.E.;
Texpression of CRYP-alpha, LAR, PTP-delta,
developing xenopus visual system.";
Mech. Dev. 92:291-294(2000).
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InterPro; IPR000242;
pfam; PF00041; fn3; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-8355;
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SEQUENCE
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l Similarity
27; Conserv
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PS50060; MAM_2; 1.
PS00383; TYR_PHOSPHATASE_1; 1.
PS50056; TYR_PHOSPHATASE_2; 1.
PS50055; TYR_PHOSPHATASE_PTP;
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nilarity 30.0%;
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Pred.
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                Mismatches
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; Pipidae;
                       Indels
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Q9L5C3;
01-OCT-2000
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01-DEC-2001
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Lactobacillus.
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MEDLINE=20507814; PubMed=11053389;
Martinez B., Antikainen
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STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

STRAIN-2022556; PubMed=10761919;

MEDLINE-2022556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Chillingworth;

Riee S.R., Morelli G., Basham D., Brown D., Chillingworth;

Riee S.R., Morvis P., Devlin K., Feltwell T., Hamlin N., I

Davies R.M., Davis P., Moule S., Mungall K., Quail M.A.,

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 72491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TremBLrel. 15, C
01-OCT-2000 (TremBLrel. 15, L
01-DEC-2001 (TremBLrel. 19, L
HYPOTHETICAL PROTEIN NMA0510.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision;
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Pred. No. 11;
.9; Mismatches
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Westerlund-Wikstrom
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O9LXF5
PRELIMINARY; PRT; 568 AA.

O9LXF5;
O1-OCT-2000 (TrEMBLrel. 15, Created)

T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E HYPOTHETICAL 62.0 KDA PROTEIN.
N F8M21_160.
S Arabidopsis thaliana (Mouse-ear cress).
S Arabidopsis thaliana (Mouse-ear cress).
S Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
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P73777;
01-FEB-1997
01-FEB-1997
01-JUN-2000
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okum Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis Sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90909; BAA17829.1; -.
Hypothetical protein; Complete proteome.
138 AA; 14585 MW; 7753B6310931D13C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803)
Bacteria; Cyanobacteria; Chroococca.
NCBI_TaxID=1148;
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EMBL; AL162753; CABB3802.1; -.
Hypothetical protein; Complete
SEQUENCE 112 AA; 11515 MW;
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31.2%;
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Pred. No. 4
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7753B6310931D13C
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E5A9D201BF1D168A CRC64;
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annotation update)
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       a; Tracheophyta;
eudicots; Rosidae;
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Yasuda M.,
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Best Local S
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Q9IU91;
Q9IU91;
O1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TREMBLREL 19, Last annotation update)
                                                                                                                                                                                     AIDS; Coa
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SEQUENCE
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EMBL; AJ389751; CAB77485.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00013; KH-domain; 4.
SMART; SM00322; KH; 4.
PROSITE; PS50084; KH_TYPE_1;
Hypothetical protein.
SEQUENCE 568 AA; 62034 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing pusubmitted (APR-2000) to the EMBL; AL353993; CAB89337.1;
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Rudd s
                                                                                                                                                                                                                                                                                                                                                     "Predominance of subtype A and G HIV type 1 in Nigeria, geographical differences in their distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-96NG-MACSW031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; Retroid viruses; NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                     Delaporte E.;
                                                                                                                                                                                                                                                                                                                                                                                                                    Peeters M., Esu-Williams E.,
Mulanga-Kabeya C., Harry T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20179113; PubMed=10716369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004087; KH.
InterPro; IPR004088; KH_TYPE_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432
  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 TRLLVPSSRIGCILGKGGAIITEMRRMTKANIRILGKENLPKVASDDDEMVQVNFMVLLL
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S., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TALLV----TGCV-STGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVI 69
                   HHIRLTISALLTALLVTGCVSTGNVAMKEQN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFS------LQFLLSRLRYFTW
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  HGIKPVVS--
                                                                              th 12.5%; Similarity 21.2%; 25; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                protein; Glycoprotein
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328 A
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                                                                                                                                                                                       AA;
-TQLLLNGSLAEEDIVIRTENYTDNAKIIIVQLNETIEINCTRPNNNTRK
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36504
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Mayer K.F.X
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27.18;
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he EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nus type 1.
Retroviridae;
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                                                                                                                                                                                                                                                                                                                                        16:315-325(2000).
                                                                              Score 69.5; I
Pred. No. 23;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71; DB Pred. No. 30; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Vergne L.
Ibironke
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                                                                                                                                                                                                                                                                                                                                                                                                       e L.,
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                                                                                                                          15;
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                                       -QQTIEQTIIKGKTNKQE
                                                                                                                                                                                       CRC64;
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52

ISSRFGSADSI---SFMIVVIKFGHTAILAPNRWQEILSLI-ISFLWVKPYRPKNLSF -SIRFGPGQAFYATGDIIENIRQAHCNV-SRTKWNEMIQKVKVQLRKIESFKNKNISF

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Best Local
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q901A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular epidemiology of HIV-1 in Portugal: subtypes in Lisbon.";
                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 58.8 KDA PROTEIN.
F21F8.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2000) to the EMBL; AJ296262; CAC82697.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canas-Ferreira W.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Esteves A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Wilson R., Favello A., Le T.T.;
Wilson R., Favello A., Le T.T.;
"The sequence of C. elegans cost
Submitted (APR-1997) to the EMB.
                                                                                                                                                                                                                                                                                     001537;
                                                                                                                                                                                                                                                                                                 001537
                                                                                                                                          STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                    NCBI_TaxID=6239;
  SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                  None;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                                                                                                                                                     SISEGPGQAFYATGDIIGNIRKAHCTI---NRTEWEKMIQNVTQKL--KETFKKNITF 151
                                                                                                                                                                                                                                                                                                                                                                    SISF-----MIVVIKEGHTAILAPNR--WQEILSLIISFLWVKPYRPKNLSF
                                                                                                                                                                                                                                                                                                                                                                                              HGIKPVVS---TQLLLNGSLAEGNITIRSENITNNAKTIIVQLKEAVNITCIRPSNNTRK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
32; Conserv
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1 (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
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168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18373 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69; DB
Pred. No. 12;
20; Mismatches
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                                     cosmid F21F8.";
EMBL/GenBank/DDBJ
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12;
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 168;
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                                                                                                                 Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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Q9KZZ5
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"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Simited (Aug-2001) to the EMBL/GenBank/DDBJ databases.
subcellular LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
-!- SUGAR TRANSPORTER FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
DUTATIVE INTEGRAL MEMBRANE!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KZZ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
Cerdeno A.M., Parkhill J., E
Submitted (APR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliver K., Harris D.;
Submitted (APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
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                                                                                                                                                                                                                                                      the 8 mb Streptomyces coelicolor A3(2) chromoson mol. microbiol. 21:77-96(1996).

EMBL; AL3538L5; CAB88438.1;

Interpro; IPR000566; Lipocln_cytFABP.

PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.

SEQUENCE 169 AA; 18814 MW; B7685780EC402D77
                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M., Der
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 HIRLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSAD----
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LTISALLTALLV--TGCVSTGNVAMKEONQQTIEQTIIKGKTNKQE-----ISSREGSA 59
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                                                                                              12.3%;
nilarity 24.0%;
Conservative 2
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Pred. No. 45;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
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                                                                                                        20;
                                                                                                     Score 68.5; Depred. No. 14; No. 14; Mismatches
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lor A3(2) cl
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      Query Match
Best Local Similarity
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O00947;

O1-JUL-1997 (TrEMBLrel. 04, C

O1-JUL-1997 (TrEMBLrel. 04, L

O1-DEC-2001 (TrEMBLrel. 19, L

TETRASKELETAL (FRAGMENT).
                                                                                                                                                                                                                                                                                    O84574 PRELIMINARY;
O84574;
O1-NOV-1998 (TrEMBLrel. 0
O1-NOV-1998 (TrEMBLrel. 0
O1-DEC-2001 (TrEMBLrel. 1
GEN. SECRETION PROTEIN F.
GSPF OR CT570.
Chlamydda trachomatis.
Bacteria; Chlamydiales; C
NCBI_TaxID-813;
                                                                                                                                                                           MEDLINE-99000809; PubMed-9784136; Stephens R.S., Kalman S., Lammel C. Mitchell W.P., Olinger L., Tatusov Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Tetrahymena vorax.";
Submitted (MAX-1997) the EMBL/Ger
EMBL; AF003091; AAB61407.1; -.
InterPro; IPR003015; HLH_Myc.
PROSITE; PS00038; HELIX_LOOP_HELIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                             Science 282:754-759(1998).
EMBL; AE001327; AAC68172.1; -.
INTERPO; IPR001992; Bact_secr_systII.
Pfam; PF00482; GSPII_F; 1.
Complete proteome.
SEQUENCE 391 AA; 43557 MW; 7785601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-C1;
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green M.
                                                                                                                                                     Chlamydia
                                                                                                                                                     "Genome sequence of an obligate intracellular Chlamydia trachomatis.";
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17; Conser
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21.7%;
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-WETAAALVLIWATWLWIR
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Pred. No. 35;
7; Mismatches
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Last annotation update)
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Q., Koonin
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                                                                  CRC64;
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Matches 26
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MITANDA
NGUYEN M., Karlin-Neumann G., Southwick A., Lam B., Miranda
Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda
Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Kamiya A.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE PLASMINOGEN ACTIVATOR INHIBITOR-1 (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eurammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                         Q94B61;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and Expression of Rabbit PAI-1.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
-!-SIMILARITY: BELONGS TO THE SERPIN FAMILY.
EMBL; AF074325; AAC62632.1; -.
HSSP; P05121; 1A7C.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yin J., Idell S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LUNG
                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                             UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                  QLTLLLLVNALYFNGQWKT----
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Last sequence
Last anno
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Pred. No. 17;
L3; Mismatches
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annotation update)
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                                                        Chen H.
                                       A., Kawai J.,
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AC P87977
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Best Local Similarity 28.8
Matches 17; Conservative
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Search completed: July 30, 2002, 15:42:33 Job time: 217 sec
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Best Local Similarity 28.0%;
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P87977;
P87977;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENVELOPE GLYCOPROTEIN, V1-V5 REGION (FRAGMENT).
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"Comparison of HIV-1 env (VI-v5) sequences from dorsal root ganglia
with sequences from brain, blood, CSF, and spinal cord from patients
who died with AIDS.";
submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U25257; AAB39463.1; ... InterPro; IPR000777; GP120. Pfam; PF00516; GP120; 1. ALDS; Coat protein; Glycoprotein.
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SEQUENCE
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                                                                                                                                                   GVHLGPGSAFYTTGEVIGDIRRGHCNISRPN-WTNTLGQIAGKLRVQ 243
                                                                                                                                                                                                      EISSREGSA-DSISEMIVVIKEGHTAILAPNRWOEILSLIISELWVK 96
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39682 MW; 96AD9399192EA9AA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                      %; Score 68; DB 15; Length 360; B; Pred. NO. 37; 16; Mismatches 43; Indels
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RESULT
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AAB60640;
                                                      AAB60640 standard; Protein; 111 AA.
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Matches

Similarity

Conservative

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1 MLNHHIRLTISALLTALLYTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSAD 60

Indels

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Gaps

0

60

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The invention relates to the Moraxella catarrhalis strain ATCC43617
CC BASB122 and BASB124 proteins (AAB60640 and AAB60641, respectively)
CC and to DNA encoding them (AAF59779 and AAF59779, respectively). The invention also relates to immunogenic fragments of the BASB122 and CC Invention also relates to immunogenic fragments of the BASB122 and CC BASB124 proteins, expression vectors and host cells comprising BASB122 or BASB124, vaccine compositions comprising the BASB122 or BASB122 or CC COMPOSITIONS (The recombinant production of BASB122 or CC COMPOSITIONS (The recombinant production of BASB124 proteins or nucleic acids, an antibody against BASB122 or BASB124, therapeutic CC compositions comprising an ABSB122 or anti-BASB124 antibody, and a CC method of identifying a Moraxella catarrhalis infection via the CC detection of BASB122 or BASB124 proteins or antibodies. The vaccine CC agents against Moraxella catarrhalis infections in mammals, particularly CC humans. Moraxella catarrhalis is a Gram negative bacterium frequently continued from the human upper respiratory tract, which is responsible for Several pathological conditions. It is responsible for about 15% of CC totits media cases in children (which can lead to temporary or permanent CC hearing loss). It also causes pneumonia in elderly people, and sinusitis, nosocomial infections and, less frequently, invasive diseases. BASB122 or CC BASB124 proteins or nucleotides may additionally be used in screening for infections. The present sequence represents the Moraxella catarrhalis cCC strain ATCC43617 BASB122 protein.
                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New BASB122 and BASB124 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines against bacterial infections, e.g. otitis media or pneumonia \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-159874/16.
N-PSDB; AAF59778.
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30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASB122 protein; strain ATCC43617; antigen; antibody; vaccine; genetic immunisation; infection; upper respiratory tract; otit hearing loss; deafness; pneumonia; sinusitis; nosocomial infec
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 66; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invasive disease; antibacterial; auditory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis strain ATCC43617 BASB122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99GB-0018034.
99GB-0018036.
100.0%; Score 111; DB 22; 100.0%; Pred. No. 3.8e-111; 7ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sinusitis; nosocomial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                           Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tract; otitis media;
```

Search completed: July 30, 2002, 15:43:08 Job time: 227 sec

us-10-048-197-2.oligo.rag

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Page 2

```
Title:
Perfect score:
Sequence:
                                                                 Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
No matches found
                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               Query
Score Match Length DB
                                                                                                                                                                                                                                                              Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIGO Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    July 30, 2002, 15:39:51; Search time 13.05 Seconds (without alignments) 207.758 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-048-197-2
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLNHHIRLTISALLTALLVT......FLWVKPYRPKNLSFYLTAKA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                 ij
                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                               Description
```

Search completed: July 30, 2002, 15:43:27 Job time: 216 sec

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

Title: Perfect score: Sequence:

US-10-048-197-2 111 1 MLNHHIRLTISALLTALLUT......FLWVKPYRPKNLSFYLTAKA 111

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 15

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB

IJ

Description

No matches found

Search completed: July 30, 2002, 15:43:50 Job time: 124 sec

1

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

July 30, 2002, 15:43:31; Search time 11.9 Seconds (without alignments) 361.166 Million cell updates/sec

Title: Perfect score: Sequence: US-10-048-197-2 111 1 MLNHHIRLTISALLTALLUT.....FLWVKPYRPKNLSFYLTAKA 111

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

105224 seqs, 38719550 residues

Word size : 15 Searched:

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB ID Description

No matches found

Result No.

Search completed: July 30, 2002, 15:47:02 Job time: 211 sec

```
GenCore version 4.5

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OM protein - protein search, using sw model

Run on:

July 30, 2002, 15:43:11; Search time 24.65 Seconds (without alignments)
779.004 Million cell updates/sec

Title:
Perfect score:
111
Sequence:
111
Scoring table:
OLIGO
Gapop 60.0, Gapext 60.0
Searched:
562222 seqs, 172994929 residues

Word size:
15
```

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: SPTREMBL_19:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_archeap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description
No matches found

Search completed: July 30, 2002, 15:46:44 Job time: 213 sec

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